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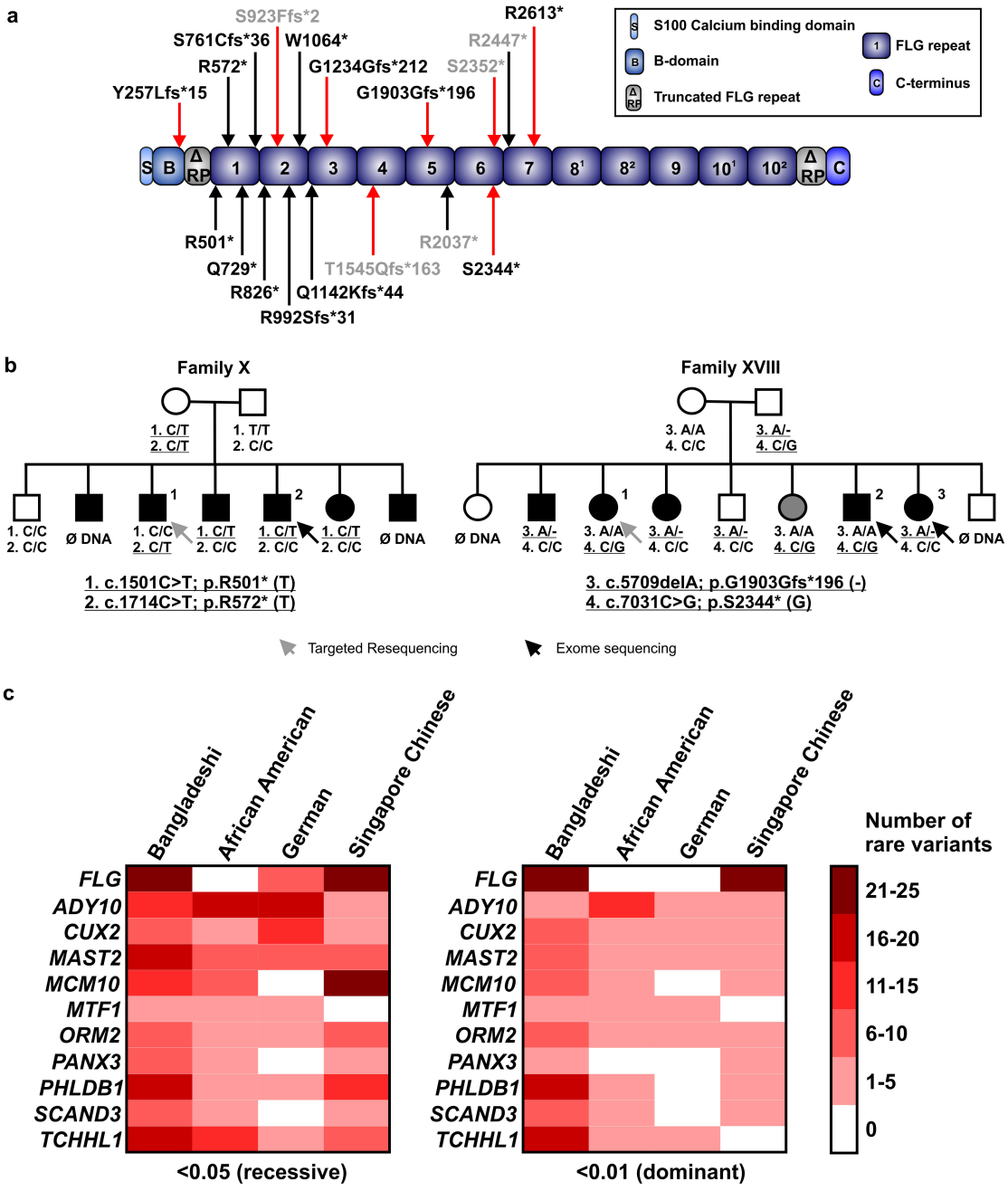

Figure 1: Filaggrin (*FLG*) risk variants identified in the Bangladeshi atopic eczema (AE) cohort and novel risk genes.

(a) Schematic representation of *FLG* showing all loss-of-function variants identified in this study. (Red arrows indicate previously unreported variants, variants shown black and gray were identified using whole exome sequencing or targeted re-sequencing, respectively) **(b)**

Exome and targeted resequencing demonstrated an intrafamilial heterogeneity of *FLG* risk variants in the Bangladeshi AE cohort, segregating, in part, within families. Of note, the parents and the oldest sibling (all unaffected) of both families were born in Bangladesh. All other siblings were born in the UK. (Black symbols indicate affected individuals, gray circle indicates a previously affected daughter, white symbols represent unaffected individuals) **(c)** Heat Maps showing the number of rare variants identified in the different AE cohorts from this study. Data are based on allele frequencies from ethnically-matching subpopulations obtained from the genomic database ExAC. Recessive and dominant variants were considered rare if they had an allele frequency <0.05 and <0.01, respectively. Filaggrin (*FLG*) loss-of-function variants were excluded in the African-American cohort as described previously (Margolis et al., 2014).